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results of BLAST

BLASTP 2.2.5 [Nov-16-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1046895000-05007-6664

Query=

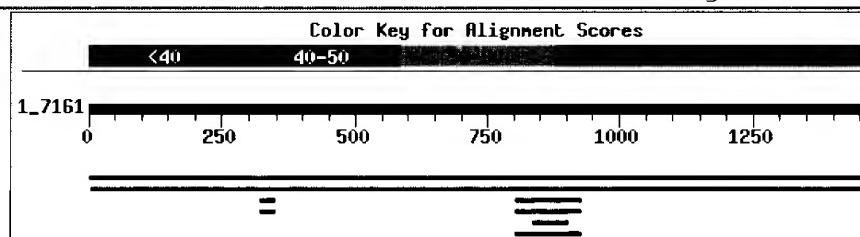
(1469 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,348,542 sequences; 431,791,111 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 8 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments: Score E
(bits) Value

gi 23396465 sp Q961D9 BCL9_DROME	Bcl-9 homolog (Legless pro...	2076	0.0	L
gi 19550445 gb AAL91368.1 AF457205_1	legless [Drosophila me...	2069	0.0	
gi 8132999 gb AAF73447.1 AF263836_1	voltage-gated potassium...	39	0.58	L
gi 23593633 ref XP_129704.2	potassium voltage-gated channe...	39	0.62	
gi 27672780 ref XP_224941.1	similar to MAP/microtubule aff...	37	3.0	
gi 23396460 sp O00512 BCL9_HUMAN	B-cell lymphoma 9 protein ...	36	6.0	
gi 4757846 ref NP_004317.1	B-cell CLL/lymphoma 9 [Homo sap...	36	6.2	L
gi 26328813 dbj BAC28145.1	unnamed protein product [Mus mu...	35	9.5	

Alignments

gi|23396465|sp|Q961D9|BCL9 DROME Bcl-9 homolog (Legless protein)
 gi|22759407|gb|AAF59345.2| CG2041-PA [Drosophila melanogaster]
 gi|21356901|ref|NP_651922.1| CG2041-PA [Drosophila melanogaster]
 gi|15291613|gb|AAK93075.1| LD02061p [Drosophila melanogaster]
 Length = 1469

Score = 2076 bits (5379), Expect = 0.0
 Identities = 1260/1469 (85%), Positives = 1260/1469 (85%)

Query: 1 MLSTTMRSPQQPQXXXXXXXXXXXXXXXIGNGDSAASRSPKTLNSEPFSTLSP 60
 MLSTTMRSPQQPQ IGGNGDSAASRSPKTLNSEPFSTLSP
 Sbjct: 1 MLSTTMRSPQQPQPNSDASSTSASGSNPGAAIGNGDSAASRSPKTLNSEPFSTLSP 60

Query: 61 DQIKLTPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTTINSCLVAXXXX 120
 DQIKLTPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTTINSCLVA
 Sbjct: 61 DQIKLTPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTTINSCLVASPQNS 120

Query: 121 XXXXXXXXXXXXATVGLTQMVDCEQSKKNCVKDEEAEISSNKAKGQAAGGGCETGSTSS 180
 ATVGLTQMVDCEQSKKNCVKDEEAEISSNKAKGQAAGGGCETGSTSS
 Sbjct: 121 SEHSNNSNVSATVGLTQMVDCEQSKKNCVKDEEAEISSNKAKGQAAGGGCETGSTSS 180

Query: 181 LTVKEEPTDVLSLVNMKKEERENHSPTMSPVGFGSIGNAQDNSATPVKIERISNDSTTE 240
 LTVKEEPTDVLSLVNMKKEERENHSPTMSPVGFGSIGNAQDNSATPVKIERISNDSTTE
 Sbjct: 181 LTVKEEPTDVLSLVNMKKEERENHSPTMSPVGFGSIGNAQDNSATPVKIERISNDSTTE 240

Query: 241 KKGSSLTMNNDEMSMEGCNQLNPDFINESLNNPAISSILVSXXXXXXXXXXXXNL 300
 KKGSSLTMNNDEMSMEGCNQLNPDFINESLNNPAISSILVS NL
 Sbjct: 241 KKGSSLTMNNDEMSMEGCNQLNPDFINESLNNPAISSILVSGVGPIPGIGVGAGTGNNL 300

Query: 301 XXXXXXXXXXXXCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL 360
 CLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL
 Sbjct: 301 ANANGISSLNCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL 360

Query: 361 EDFFMKNPLKINKLQRHNSVGMPIGMGVGLTPNPVAKITQQQPHTKTVGLLPQFNQ 420
 EDFFMKNPLKINKLQRHNSVGMPIGMGVGLTPNPVAKITQQQPHTKTVGLLPQFNQ
 Sbjct: 361 EDFFMKNPLKINKLQRHNSVGMPIGMGVGLTPNPVAKITQQQPHTKTVGLLPQFNQ 420

Query: 421 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSESQ 480
 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSESQ
 Sbjct: 421 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSESQ 480

Query: 481 AIKILEAAGVDLGVTKGSDPGLTENNIVSLQGVKVPDENLTPQQRHREEQLAKIKM 540
 AIKILEAAGVDLGVTKGSDPGLTENNIVSLQGVKVPDENLTPQQRHREEQLAKIKM
 Sbjct: 481 AIKILEAAGVDLGVTKGSDPGLTENNIVSLQGVKVPDENLTPQQRHREEQLAKIKM 540

Query: 541 NQFLFPENENSGANVSSQITKIPGDLXXXXXXXXXXINPTMRQLHMPGNNAKSELLSA 600
 NQFLFPENENSGANVSSQITKIPGDL ININPTMRQLHMPGNNAKSELLSA
 Sbjct: 541 NQFLFPENENSGANVSSQITKIPGDLMMGMSGGGGSIINPTMRQLHMPGNNAKSELLSA 600

Query: 601 TSSGLSEDVMHPGDVISDMGAVIGCANNQKTSVQCGSXXXXXXXXXXMHCSSSG 660
 TSSGLSEDVMHPGDVISDMGAVIGCANNQKTSVQCGS MHCSSSG
 Sbjct: 601 TSSGLSEDVMHPGDVISDMGAVIGCANNQKTSVQCGSGVGVTTAGVNVMHCSSSG 660

Query: 661 APNGNMMGSSTDMLASFGNTCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIHQ 720
 APNGNMMGSSTDMLASFGNTCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIHQ
 Sbjct: 661 APNGNMMGSSTDMLASFGNTCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIHQ 720

Query: 721 FFEERLKGGXXXXXXXXXXXXSGGGNSLNNQVRPLQGPPPPYHSIQRASVPIAT 780
 FFEERLKGGK SGSGGNSLNNQVRPLQGPPPPYHSIQRASVPIAT
 Sbjct: 721 FFEERLKGGKPRQVTGTVVPQQTPSGGGNSLNNQVRPLQGPPPPYHSIQRASVPIAT 780

Query: 781 QXXXXXXXXXXXXRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA 840
 Q RTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA
 Sbjct: 781 QSPNPSSPNNLSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA 840

Query: 841 NKNCFQADTPSPSNQNRSRNTGSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMK 900
 NKNCFQADTPSPSNQNRSRNTGSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMK
 Sbjct: 841 NKNCFQADTPSPSNQNRSRNTGSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMK 900

 Query: 901 SRRPSPQGQRSPVNSLIEANKDVRFAASSPGFNPHPMQSNSNSALNAYKMGSTNIQMER 960
 SRRPSPQGQRSPVNSLIEANKDVRFAASSPGFNPHPMQSNSNSALNAYKMGSTNIQMER
 Sbjct: 901 SRRPSPQGQRSPVNSLIEANKDVRFAASSPGFNPHPMQSNSNSALNAYKMGSTNIQMER 960

 Query: 961 QASAQGGSVQFSRRSDNIPLNPNNSGNRPPPKMTQNFDPPISSLAQMSQQLTSCVXXXXXX 1020
 QASAQGGSVQFSRRSDNIPLNPNNSGNRPPPKMTQNFDPPISSLAQMSQQLTSCV
 Sbjct: 961 QASAQGGSVQFSRRSDNIPLNPNNSGNRPPPKMTQNFDPPISSLAQMSQQLTSCVSSMGSP 1020

 Query: 1021 XXXXXXXXXXXXXXXXNIEHXXXXXXXXXXXXXNQNNCHSMNVVMNSMGPRMLNPKMC 1080
 DINTEH NQNNCHSMNVVMNSMGPRMLNPKMC
 Sbjct: 1021 AGTGGMTMMGGPGPSDINIEHGIISGLDGSGIDTINQNNCHSMNVVMNSMGPRMLNPKMC 1080

 Query: 1081 VAXXXXXXXXXXXXXXXLRENSIGSGCGSANSSNFQGVVPPGARMMGRMPVNFGSNFN 1140
 VA LRENSIGSGCGSANSSNFQGVVPPGARMMGRMPVNFGSNFN
 Sbjct: 1081 VAGGPNGPPGFNPNSPNGGLRENSIGSGCGSANSSNFQGVVPPGARMMGRMPVNFGSNFN 1140

 Query: 1141 PNIQVKASTPNTIQYMPVRAQXXXXXXXXXVRMPPSLEFLQRYANPQMGAVGNGSPI 1200
 PNIQVKASTPNTIQYMPVRAQ VRMPPSLEFLQRYANPQMGAVGNGSPI
 Sbjct: 1141 PNIQVKASTPNTIQYMPVRAQNANNNNNGANNVRMPPSLEFLQRYANPQMGAVGNGSPI 1200

 Query: 1201 CPPSASDGTXXXXXXXXXXXXXNNSGEQHQNKITNNPGASNGINFFQNCNQMSIVD 1260
 CPPSASDGT NSSGEQHQNKITNNPGASNGINFFQNCNQMSIVD
 Sbjct: 1201 CPPSASDGTGMPGLMAGPGAGGMLMNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVD 1260

 Query: 1261 EEGGLPGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPVNRQIQQFAQSSDGIDCVGDPS 1320
 EEGGLPGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPVNRQIQQFAQSSDGIDCVGDPS
 Sbjct: 1261 EEGGLPGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPVNRQIQQFAQSSDGIDCVGDPS 1320

 Query: 1321 SFFTNASCNSAGPHMFSAQQANQPKTQHIKNIPSGMCQNCQNSGLAVAQQQIQLHGQGHAQ 1380
 SFFTNASCNSAGPHMFSAQQANQPKTQHIKNIPSGMCQNCQNSGLAVAQQQIQLHGQGHAQ
 Sbjct: 1321 SFFTNASCNSAGPHMFSAQQANQPKTQHIKNIPSGMCQNCQNSGLAVAQQQIQLHGQGHAQ 1380

 Query: 1381 GQSLIGPTNNNLSTMAGVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNTRSXX 1440
 GQSLIGPTNNNLSTMAGVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNTRS
 Sbjct: 1381 GQSLIGPTNNNLSTMAGVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNRSQQ 1440

 Query: 1441 XXXXXXXXSNMITMPPNLSPNPTFFVNK 1469
 SNMITMPPNLSPNPTFFVNK
 Sbjct: 1441 QQHMHQHQSNMITMPPNLSPNPTFFVNK 1469

|>gi|19550445|gb|AAL91368.1|AF457205_1 legless [Drosophila melanogaster]
 Length = 1464

Score = 2069 bits (5360), Expect = 0.0
 Identities = 1255/1464 (85%), Positives = 1255/1464 (85%)

Query: 6 MPRSPTQQQPXXXXXXXXXXXXXXXXXIGNGDSAASRSSPKTLNSEPFSTLSPDQIKL 65
 MPRSPTQQQPQ IGNGDSAASRSSPKTLNSEPFSTLSPDQIKL
 Sbjct: 1 MPRSPTQQQPQPNSDASSTSASGSNPGAAIGNGDSAASRSSPKTLNSEPFSTLSPDQIKL 60

Query: 66 TPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSCLVXXXXXXXXX 125
 TPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSCLVA
 Sbjct: 61 TPEEGTEKGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSCLVASPQNSSEHSN 120

Query: 126 XXXXXATVGLTQMVDCEQSCKKNKCSVKDEEAEISSNKAKGQAAGGGCETGSTSSLTVKE 185
 ATVGLTQMVDCEQSCKKNKCSVKDEEAEISSNKAKGQAAGGGCETGSTSSLTVKE
 Sbjct: 121 SSNVSATVGLTQMVDCEQSCKKNKCSVKDEEAEISSNKAKGQAAGGGCETGSTSSLTVKE 180

Query: 186 EPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTEKKGSS 245
 EPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTEKKGSS
 Sbjct: 181 EPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTEKKGSS 240

Query: 246 LTMNNDEMSMEGCNQLNPDFINESLNNPAISSLVXXXXXXXXXXXXXNLLTXXXXX 305
Sbjct: 241 LTMNNDEMSMEGCNQLNPDFINESLNNPAISSLV NLLT
Query: 306 XXXXXXCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSLEDFFM 365
Sbjct: 301 ISSGSSNCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSLEDFFM 360
Query: 366 KNPLKINKLQRHNSVGMPWIGMGQVGLTPPNPVAKITQQQPHTKTVGLLKPQFNQHENSK 425
Sbjct: 361 KNPLKINKLQRHNSVGMPWIGMGQVGLTPPNPVAKITQQQPHTKTVGLLKPQFNQHENSK 420
Query: 426 RSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSESQAIIKIL 485
Sbjct: 421 RSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSESQAIIKIL 480
Query: 486 EAAGVDLGQVTKGSDPGLTENNIVSLQGVKVPDENLTPQQRQHREEQLAKIKKMNQFLF 545
Sbjct: 481 EAAGVDLGQVTKGSDPGLTENNIVSLQGVKVPDENLTPQQRQHREEQLAKIKKMNQFLF 540
Query: 546 PENENSGGANVSSQITKIPGDLXXXXXXXXXXIINPTMRQLHMPGNAKSELLSATSSGL 605
Sbjct: 541 PENENSGGANVSSQITKIPGDLMMGMMSGGGGSIIINPTMRQLHMPGNAKSELLSATSSGL 600
Query: 606 SEDVMHPGDVISDMGAVIGCNNNQKTSVQCGSXXXXXXXXXXXXMHCSSGAPNGN 665
Sbjct: 601 SEDVMHPGDVISDMGAVIGCNNNQKTSVQCGS MHCSSGAPNGN
Query: 666 MMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMMEWSKIQHQFFER 725
Sbjct: 661 MMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMMEWSKIQHQFFER 720
Query: 726 LKGGKXXXXXXXXXXXXXSGSGGNSLNQVRPLQGPPPPYHSIQRSASVPIATQXXX 785
Sbjct: 721 LKGGK SGSGGNSLNQVRPLQGPPPPYHSIQRSASVPIATQ
Query: 786 XXXXXXXXXXXRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANKCF 845
Sbjct: 781 SSPNNLSPSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANKCF 840
Query: 846 QADTPSPSNQNRNRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMKSRP 905
Sbjct: 841 QADTPSPSNQNRNRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMKSRP
Query: 906 PQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQNSNSALNAYKMGSTNIQMERQASAQ 965
Sbjct: 901 PQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQNSNSALNAYKMGSTNIQMERQASAQ 960
Query: 966 GGSVQFSRRSDNIPLNPNNSGNRPPPQKMTQNFDPISSLAQMSQQLTSCVXXXXXXXXX 1025
Sbjct: 961 GGSVQFSRRSDNIPLNPNNSGNRPPPQKMTQNFDPISSLAQMSQQLTSCVSSMGSPACTGG 1020
Query: 1026 XXXXXXXXXXXXIDINIEXXXXXXXXXXXXXNQNNCHSMNVVMNSMGPRMLNPKMCVAXXX 1085
Sbjct: 1021 DINIEH NQNNCHSMNVVMNSMGPRMLNPKMCVA
MTMMGGPGPSDINIEHGIISGLDGSGIDTINQNNCHSMNVVMNSMGPRMLNPKMCVAGGP 1080
Query: 1086 XXXXXXXXXXXXXLRENSIGSGCGSANSSNFQGVVPPGARMGRMPVNFGSNFPNIQV 1145
Sbjct: 1081 LRENSIGSGCGSANSSNFQGVVPPGARMGRMPVNFGSNFPNIQV
NGPPGFNPNSPNGGLRENSIGSGCGSANSSNFQGVVPPGARMGRMPVNFGSNFPNIQV 1140
Query: 1146 KASTPNTIQYMPVRAQXXXXXXXXXXXXXVRMPPSLEFLQRYANPQMGAVGNGSPICPPSA 1205
Sbjct: 1141 KASTPNTIQYMPVRAQNANNNNNGANNVRMPPSLEFLQRYANPQMGAVGNGSPICPPSA 1200

Query: 1206 SDGTXXXXXXXXXXXXXXNNSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL 1265
 SDGT NSSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL

Sbjct: 1201 SDGTPGMPGLMAGPGAGGMLMNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL 1260

Query: 1266 PGHDGSMMIQQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFTN 1325
 PGHDGSMMIQQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFTN

Sbjct: 1261 PGHDGSMMIQQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFTN 1320

Query: 1326 ASCNSAGPHMFGBAQQQANQPKTQHIKNIPSGMCQNQSGLAVAQQQIQLHGQGHAQQQSLI 1385
 ASCNSAGPHMFGBAQQQANQPKTQHIKNIPSGMCQNQSGLAVAQQQIQLHGQGHAQQQSLI

Sbjct: 1321 ASCNSAGPHMFGBAQQQANQPKTQHIKNIPSGMCQNQSGLAVAQQQIQLHGQGHAQQQSLI 1380

Query: 1386 GPTNNNLSTMAGSVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNTRSXXXXXX 1445
 GPTNNNLSTMAGSVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNTRS

Sbjct: 1381 GPTNNNLSTMAGSVSATNGVSGINFVGPSSTDLKYAQQYHSFQQQLYATNRSQQQHMH 1440

Query: 1446 XXXXSNNMITMPPNLSPNPTFFFVNK 1469

SNMITMPPNLSPNPTFFFVNK

Sbjct: 1441 QQHQSNNMITMPPNLSPNPTFFFVNK 1464

gi|8132999|gb|AAF73447.1|AF263836_1 L voltage-gated potassium channel KCNQ5 [Mu
 gi|14285398|sp|Q9JK45|CIQ5_MOUSE Potassium voltage-gated channel subfamily KQT me
 channel KQT-like 5)
 Length = 878

Score = 38.9 bits (89), Expect = 0.58

Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLGSPQANTSTVQAGTTVLSANK---NCFQADTPSPSNQNR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S

Sbjct: 606 PVDSKDLGSAQNSGCLTRSASANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPMS 665

Query: 859 RNTGSSSVLTHNLSSN-----PSTPLSHLSPKEFESFGQSSAGDNMKSRPSPQGQRSP 912
 +N GSS V T+N++ P+ P+ P + S + + S Q S

Sbjct: 666 QNDGSSVVATNNIANQISAAPKPAAPTLQIPPPLSAIKHLSRPEPLSNPTGLQESISD 725

Query: 913 VNSLIEANKD-VRFAASS 929

V + + A+K+ V+FA S+

Sbjct: 726 VTTCLVASKESVQFAQSN 743

gi|23593633|ref|XP_129704.2| potassium voltage-gated channel, subfamily Q, membr
 musculus]
 Length = 846

Score = 38.9 bits (89), Expect = 0.62

Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLGSPQANTSTVQAGTTVLSANK---NCFQADTPSPSNQNR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S

Sbjct: 574 PVDSKDLGSAQNSGCLTRSASANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPMS 633

Query: 859 RNTGSSSVLTHNLSSN-----PSTPLSHLSPKEFESFGQSSAGDNMKSRPSPQGQRSP 912
 +N GSS V T+N++ P+ P+ P + S + + S Q S

Sbjct: 634 QNDGSSVVATNNIANQISAAPKPAAPTLQIPPPLSAIKHLSRPEPLSNPTGLQESISD 693

Query: 913 VNSLIEANKD-VRFAASS 929

V + + A+K+ V+FA S+

Sbjct: 694 VTTCLVASKESVQFAQSN 711

gi|27672780|ref|XP_224941.1| similar to MAP/microtubule affinity-regulating kir
 ELKL motif kinase 1; ELKL motif kinase [Homo sapiens]
 [Rattus norvegicus]
 Length = 654

Score = 36.6 bits (83), Expect = 3.0

Identities = 18/68 (26%), Positives = 33/68 (48%), Gaps = 8/68 (11%)

Query: 838 LSANKNCFQADTPSPSNQNRSRNTGSSVLTNLSSNPSTPLSHLSPKEFESFGQSSAGD 897
 +S NCF N++ S N G +++ H + ++P+ + P+ +SFG SA +
 Sbjct: 421 ISPTLNCF-----NKSESLNKGKRTIVRHTMPPKKTSPVRRICPRLHKSFGMGSASE 472

Query: 898 NMKSRRPS 905
 + R S
 Sbjct: 473 DSSKRNNS 480

l>gi|23396460|sp|O00512|BCL9_HUMAN B-cell lymphoma 9 protein (Bcl-9) (Legless hor
 Length = 1426

Score = 35.8 bits (81), Expect = 6.0
 Identities = 16/28 (57%), Positives = 25/28 (89%)

Query: 323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
 ++VFST++ANK AE+VL GQ +TI+++H
 Sbjct: 177 VYVFSTEMANKAAEAVLKGQVETIVSFH 204

l>gi|4757846|ref|NP_004317.1| B-cell CLL/lymphoma 9 [Homo sapiens]
gi|2570024|emb|CAA73942.1| B-cell CLL/lymphoma 9 [Homo sapiens]
 Length = 1394

Score = 35.8 bits (81), Expect = 6.2
 Identities = 16/28 (57%), Positives = 25/28 (89%)

Query: 323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
 ++VFST++ANK AE+VL GQ +TI+++H
 Sbjct: 177 VYVFSTEMANKAAEAVLKGQVETIVSFH 204

l>gi|26328813|dbj|BAC28145.1| unnamed protein product [Mus musculus]
 Length = 572

Score = 35.0 bits (79), Expect = 9.5
 Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLSGSVPQANTSTVQAGTTVLSANK---NCFQADTPSPSNQR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S
 Sbjct: 300 PVDSKDLGSAQNSGCLTRSASANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPM 359

Query: 859 RNTGSSSVLTHNLSSN----PSTPLSHLSPKEFESFGQSSAGDNMKSRPSPQQQRSP 912
 +N GSS V T+N++ P+ P+ P + S + + S Q S
 Sbjct: 360 QNDGSSVVATNNIANQISAAPKPAAPTLQIPPLSAIKHLSRPEPLSNPTGLQESISD 419

Query: 913 VNSLIEANKD-VRFAASS 929
 V + + A+K+ V+FA S+
 Sbjct: 420 VTTCLVASKESVQFAQSN 437

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

Posted date: Feb 26, 2003 10:23 PM

Number of letters in database: 431,791,111

Number of sequences in database: 1,348,542

Lambda K H
 0.309 0.125 0.356

Gapped
 Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1,110,058,764
Number of Sequences: 1348542
Number of extensions: 43687358
Number of successful extensions: 111049
Number of sequences better than 10.0: 267
Number of HSP's better than 10.0 without gapping: 24
Number of HSP's successfully gapped in prelim test: 258
Number of HSP's that attempted gapping in prelim test: 108537
Number of HSP's gapped (non-prelim): 1637
length of query: 1469
length of database: 431,791,111
effective HSP length: 136
effective length of query: 1333
effective length of database: 248,389,399
effective search space: 331103068867
effective search space used: 331103068867
T: 11
A: 40
X1: 16 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 79 (35.0 bits)